



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 123751

To: Christopher Yaen
Location: REM/3A20/3C18
Art Unit: 1642
Wednesday, June 09, 2004

Case Serial Number: 09/538106

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Christopher,

This request was not forwarded to Ed Hart. It was placed in the "general pool" of incoming searches. I processed prior to reading CC: addressee.

Beverly

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 06-09-04
Searcher: Beverly C 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Type

- STIC
- CM-1
- Pre-S
- N.A. Sequence
- A.A. Sequence
- Structure
- Bibliographic

Vendors

- IG
- STN
- Dialog
- APS
- Geninfo
- SDC
- DARC/Questel
- Other

| | | | |
|------------|--------|--|---|
| US-09-538- | 178 | DVSTQOSSTAKSATWTYSTELKKLYCQI | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 139 | DVSQOSSTAKSATWTYSTELKKLYCQI | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 84 | DVSQOSSTAKSATWTYSTELKKLYCQI | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 84 | DVSQOSSTAKSATWTYSTELKKLYCQI | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 64 | ALSPSPATPSNTDYPGPSPFDISQOSSTAKSATWTYSTELKKLYCQIAKTCPQIKWMP | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 64 | ALSPSPATPSNTDYPGPSPFDISQOSSTAKSATWTYSTELKKLYCQIAKTCPQIKWMP | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 119 | ALSPSPATPSNTDYPGPSPFDISQOSSTAKSATWTYSTELKKLYCQIAKTCPQIKWMP | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 158 | ALSPSPATPSNTDYPGPSPFDISQOSSTAKSATWTYSTELKKLYCQIAKTCPQIKWMP | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 137 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 137 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 192 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 231 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 192 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 137 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 137 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 245 | tkbindniaiftevqkrsqkeindmakavasieesegnqdk1alkbavkeitdaksrew | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 933377 | 933377 | Ykkabehvttevkkrcphnhesrefneqqiappshlirvegnshaqyvedpitgrqsvlvpye |
| consensus | | | consensus |
| US-09-538- | 231 | YKKABHVTVEVKRQPNHELSRENEQGQAPPSSHILRVEGNSHAQYVEDPITGRQSVLVPY | AKTCPQIKWTPPOGAVRAMPY |
| US-09-538- | 247 | EARICACPGDRAKADESIRKQVSDSAKNGD | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 302 | EARICACPGDRAKADESIRKQVSDSKNGD | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 341 | EARICACPGDRAKADESIRKQVSDSAKNGD | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 320 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 320 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 375 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 320 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 414 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 414 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 375 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 320 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 320 | LKIKESLIMQILOPHITBTRQQOOOHOHQILOKTSIOPSSYKANSSPLNKOMSMNK | aFRONTGQOMTSIKRSRSPDELL |
| US-09-538- | 533377 | 533377 | 428 arqeslestllslsqsgehqrlpagaleglgseadodglastvrsigetqvlvgveel |
| consensus | | | likikeslemlqipqhtietryqqgqgqgqhlqkts-qq-asyyaspplnkunsmk |
| US-09-538- | 292 | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |
| US-09-538- | 292 | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |
| US-09-538- | 253 | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |
| US-09-538- | 198 | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |
| US-09-538- | 198 | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |
| US-09-538- | 306 | dmeairstlqltmesdiytevre-lvsikqeqgafkedaetralqalgatkeklrsseasvr | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |
| consensus | | | PPQGTTETTIVLNFMCNSCYGGMNRPLPILITBTRDGOVGLGRFCEARICCPGRDR |

| | | | | |
|------------|-----|--|------------|-----|
| US-09-538- | 436 | LPSISQLINPQRAALPTIPDGMGANTPMGTHMPAGDNGLSPQALPPPLSPSTS | US-09-538- | 449 |
| US-09-538- | 381 | LPSISQLINPQRAALPTIPDGMGANTPMGTHMPAGDNGLSPQALPPPLSPSTS | US-09-538- | 484 |
| US-09-538- | 381 | LPSISQLINPQRAALPTIPDGMGANTPMGTHMPAGDNGLSPQALPPPLSPSTS | US-09-538- | 457 |
| s33377 | 489 | krsvgelpstveslqkvgeqvhllsqdqaaarlppdfdrllsionlkavsqveadl | RIMQV | |
| consensus | | lpvpsqlinqpqgnaltppt-p-gmganipmgthmpmagdnglspqalppplspsts | RIMQV | |
| US-09-538- | 365 | PRgbaptQSDVFRPHsnPPNhSYTP | US-09-538- | 551 |
| US-09-538- | 369 | PRRTPKQSDVFRPHSKPNRSTP | US-09-538- | 658 |
| US-09-538- | 424 | PRRTPKQSDVFRPHSKPNRSTP | US-09-538- | 619 |
| US-09-538- | 459 | PRgbaptQSDVFRPHsnPPNhSYTP | US-09-538- | 564 |
| US-09-538- | 442 | HCTPPPPPTDCSIV | US-09-538- | 564 |
| US-09-538- | 442 | HCTPPPPPTDCSIV | US-09-538- | 602 |
| US-09-538- | 497 | HCTPPPPPTDCSIV | US-09-538- | 551 |
| US-09-538- | 536 | HCTPPPPPTDCSIV | US-09-538- | 658 |
| US-09-538- | 536 | HCTPPPPPTDCSIV | US-09-538- | 619 |
| US-09-538- | 497 | HCTPPPPPTDCSIVSFLARCLGSSCLDYFTQGLTTIYQLEHYMSMDLASKIPEQFRHA | US-09-538- | 564 |
| US-09-538- | 442 | HCTPPPPPTDCSIVSFLARCLGSSCLDYFTQGLTTIYQLEHYMSMDLASKIPEQFRHA | US-09-538- | 564 |
| US-09-538- | 442 | HCTPPPPPTDCSIVSFLARCLGSSCLDYFTQGLTTIYQLEHYMSMDLASKIPEQFRHA | US-09-538- | 564 |
| s33377 | 550 | kmrltavalsivaysVketnemnlesakglldmlndlrlfukvekhev | US-09-538- | 551 |
| consensus | | hctppppptdcsvsf--nl---cldyftqgltyiqyehysmdlaskipeqfrha | US-09-538- | 551 |

Alignment score = -6012.00

Scoring matrix:

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|--|------|------|------|------|------|-------|------|------|-------|------|------|------|
| | -190 | -399 | -734 | -75 | -668 | -1003 | -366 | -216 | -554 | -75 | -668 | |
| | | | | -112 | -548 | 293 | -452 | -888 | 434 | -315 | -769 | 292 |
| | | | | | 76 | -314 | 168 | -264 | -315 | 313 | -147 | -321 |
| | | | | | | -646 | -44 | 108 | -747 | -123 | 219 | -648 |
| | | | | | | | -167 | -603 | 97 | -148 | -462 | 577 |
| | | | | | | | | 21 | -652 | -24 | -91 | -172 |
| | | | | | | | | | -1084 | -460 | -118 | -604 |
| | | | | | | | | | | -73 | -529 | 106 |
| | | | | | | | | | | | 91 | -148 |
| | | | | | | | | | | | | -19 |
| | | | | | | | | | | | | 10 |
| | | | | | | | | | | | | 11 |
| | | | | | | | | | | | | 12 |
| | | | | | | | | | | | | 13 |

| | | | | | |
|------------|-----|--|------------|---|-------|
| US-09-538- | 597 | IWKGILDRQLAFFSSPFPHLILTPSGASTVSGSSETGERVFDAYVFTLROTSPPPRDE | US-09-538- | 1 | -1019 |
| US-09-538- | 558 | IWKGILDRQLAFFSSPFPHLILTPSSASTVSGSSETGERVFDAYVFTLROTSPPPRDE | US-09-538- | 2 | -911 |
| US-09-538- | 503 | IWKGILDRQLAFFSSPFPHLILTPSSASTVSGSSETGERVFDAYVFTLROTSPPPRDE | US-09-538- | 3 | -289 |
| US-09-538- | 503 | IWKGILDRQLAFFSSPFPHLILTPSSASTVSGSSETGERVFDAYVFTLROTSPPPRDE | US-09-538- | 4 | 77 |
| s33377 | 602 | IWKGILDRQLAFFSSPFPHLILTPSGASTVSGSSETGERVFDAYVFTLROTSPPPRDE | | | |
| consensus | | IWKGILDRQLAFFSSPFPHLILTPSGASTVSGSSETGERVFDAYVFTLROTSPPPRDE | | | |

| | | | | | |
|------------|-----|--|------------|-----|---|
| US-09-538- | 186 | ITGRQSVLVPTEPPQGTEFTIVJINFMCHSSCCVGGMNRPILLIVTLERDGQTRGP | US-09-538- | 475 | LPSVQLINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS |
| US-09-538- | 241 | ITGRQSVLVPTEPPQGTEFTIVJINFMCHSSCCVGGMNRPILLIVTLERDGQTRGP | US-09-538- | 436 | LPSVQLINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS |
| US-09-538- | 280 | ITGRQSVLVPTEPPQGTEFTIVJINFMCHSSCCVGGMNRPILLIVTLERDGQTRGP | US-09-538- | 381 | LPSVQLINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS |
| US-09-538- | 259 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 381 | LPSVQLINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS |
| US-09-538- | 259 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 489 | Lkrsveglipstvesiqkyqeqvhtlscdqaaqr1Pqdfdariss1dnlikavsqread |
| consensus | | lpsvqlinqqrmalitptipmpegmaniipmmgthmpmagdmnglspqalpplsmsts | | | |
| US-09-538- | 314 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 365 | PRgaptosdvvfrhnsppnhsytp |
| US-09-538- | 353 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 369 | PRRETPKQSDNFVFRHNSPPNHSYTP |
| US-09-538- | 353 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 424 | PRRETPKQSDNFVFRHNSPPNHSYTP |
| US-09-538- | 314 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 459 | PRgaptosdvvfrhnsppnhsytp |
| US-09-538- | 259 | KADEDSIRKQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 442 | HCPPPPIPDCSIV |
| US-09-538- | 367 | peerirrlleelrqlkeshgpkedggfrhseafalqksgglerlqlqvvedgylsmqas | US-09-538- | 442 | HCPPPPIPDCSIV |
| consensus | | kadebsirkqqvsds-kngdgtkrfrqntgqmtsikrspddelilylpvgretem | | | |
| US-09-538- | 247 | EARICACPGDRKADEDSKRQQVSDSAKED | US-09-538- | 536 | HCPPPPIPDCSIV |
| US-09-538- | 247 | EARICACPGDRKADEDSKRQQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 536 | HCPPPPIPDCSIV |
| US-09-538- | 302 | EARICACPGDRKADEDSKRQQVSDSKNGDTRPRQNTGQMTSIKERSRSPDELYLPVGRETEM | US-09-538- | 497 | HCPPPPIPDCSIV |
| US-09-538- | 341 | EARICACPGDRKADEDSKRQQVSDSAKED | US-09-538- | 442 | HCPPPPIPDCSIV |
| US-09-538- | 320 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 442 | HCPPPPIPDCSIV |
| US-09-538- | 320 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 550 | 1kmrltavds1avsvkietnenleaskg1lddrndldr1fvkvekhev |
| US-09-538- | 375 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 550 | 1kmrltavds1avsvkietnenleaskg1lddrndldr1fvkvekhev |
| US-09-538- | 414 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 390 | hcptpppyptdcisflarlgcsscdyfroglitivoiehysmdllasjkipeoprh |
| US-09-538- | 414 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 394 | caaa49535 |
| US-09-538- | 375 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 449 | hcptpppyptdcisflarlgcsscdyfroglitivoiehysmdllasjkipeoprh |
| US-09-538- | 320 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 484 | caaa49535 |
| US-09-538- | 320 | LIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 457 | hcptpppyptdcisflarlgcsscdyfroglitivoiehysmdllasjkipeoprh |
| US-09-538- | 428 | arqteleslisksqeHeqzlaalqrlieglsheadqglastvrs1qetqylqydvree | US-09-538- | 512 | caaa49535 |
| consensus | | likikeslelmqylpqhtietryqgqgqghlqkqts - qs - a sygnsspplnknsnk | | | |
| US-09-538- | 304 | YLPVGRGTYEMLIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 551 | caaa49535 |
| US-09-538- | 308 | YLPVGRGTYEMLIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 551 | caaa49535 |
| US-09-538- | 363 | YLPVGRGTYEMLIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 558 | caaa49535 |
| US-09-538- | 398 | YLPVGRGTYEMLIKIKESLELMQYLPQHTIETYRQQQQQOHLLQKOTS1QSPSYGNSSPPLKNSNK | US-09-538- | 503 | caaa49535 |
| US-09-538- | 381 | LPSVSLQINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS | US-09-538- | 503 | caaa49535 |
| US-09-538- | 436 | LPSVSLQINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS | US-09-538- | 603 | caaa49535 |
| US-09-538- | 475 | LPSVSLQINQFQRMALITPTIPMPEGMANIIPMMGTHMPMAGDMNGLSPQALPPLSMSTS | US-09-538- | 390 | caaa49535 |

| | | | |
|------------|-----|----|-------|
| US-09-538- | 394 | 4 | 77 |
| US-09-538- | 449 | 5 | -626 |
| US-09-538- | 484 | 6 | -4 |
| US-09-538- | 457 | 7 | 362 |
| US-09-538- | 457 | 8 | -1103 |
| US-09-538- | 512 | 9 | -483 |
| US-09-538- | 551 | 10 | -91 |
| US-09-538- | 558 | 11 | -623 |
| US-09-538- | 619 | 12 | -3 |
| US-09-538- | 564 | 13 | |
| caa49535 | 603 | | |

consensus: wndlnfnfdmnd-rmnkqgrl--ge

Alignment score = -6009.00

Scoring matrix:

| | 22 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|----|------|------|------|------|------|-------|------|------|------|------|------|----|
| 22 | -185 | -404 | -739 | -80 | -673 | -1008 | -356 | -221 | -558 | -80 | -673 | |
| 2 | -112 | -548 | 293 | -452 | -888 | 434 | -315 | -769 | 292 | -457 | | |
| 3 | | 76 | -314 | 168 | -264 | -315 | 313 | -147 | -321 | 171 | | |
| 4 | | | -646 | -44 | 108 | -747 | -123 | 219 | -648 | -54 | | |
| 5 | | | | -167 | -603 | 97 | -148 | -462 | 577 | -172 | | |
| 6 | | | | | 21 | -652 | -24 | -91 | -172 | 456 | | |
| 7 | | | | | | -1084 | -460 | -118 | -604 | 20 | | |
| 8 | | | | | | | -73 | -529 | 106 | -647 | | |
| 9 | | | | | | | | 91 | -148 | -19 | | |
| 10 | | | | | | | | | -469 | -91 | | |
| 11 | | | | | | | | | | -167 | | |
| 12 | | | | | | | | | | | | |
| 13 | | | | | | | | | | | | |

13

| | |
|----|-------|
| 22 | -1024 |
| 2 | -911 |
| 3 | -289 |

PSHLIRVEGNSHAQYVEDITGRGSVLYVPEPPQVGIERT----TVL-YNFMCNSSCVGGMNRRLPILLI-
170 180 190 200 210 220 230
270 280 290 300 310 320 330
MKAVALSLESESEGKQDLKALKAEVKETQTSAKSREWDMSLARSTLQTMESDITYVEVRELVYLSIKQOOQAFK-
----VTLERTRDG--QVLRRCLEARICAPCGDRKADEDSSRKQVSDSAQNGDAFRQNTGQMTSIKR
340 350 360 370 380 390 400
EADTERLAI---QALTEKLUISSEESVSLPPEIRRLLEELRQLKSDSHGPDKEDGGFRHSBAEALQKQSQ
-RSPDDELLVLPVGRETYEMLKIKESLMLQH-TETRQQQQQH----QHLQK--
300 310 320 330 340
GLDS--RLQHVEDGVLSMQVASARQTESLESLSIKSQBHEORLAALQRLGEGLGSSSEADQGLASTV
HLLSACFRNELVLRGEAPTSQDVFRRBSNPPPHSVV
360 370 380 X
480 490
ETQLVLYGDVEELRS

2. caa49535 (1-602)
US-09-538-106-18 Sequence 18, Application US/09538106
GENERAL INFORMATION:
APPLICANT: MCKEON, FRANK
APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA
APPLICANT: CRUM, CHRISTOPHER
TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
FILE REFERENCE: HMV-038-02
CURRENT APPLICATION NUMBER: US/09/538,106
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/174,493
PRIOR FILING DATE: 1998-10-15
PRIOR APPLICATION NUMBER: 60/087,216
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/062,076
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 393
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 7 Optimized Score = 61 Significance = 2.40
Residue Identity = 19% Matches = 83 Mismatches = 278
Gaps = 69 Conservative Substitutions = 0

10 20 30 40 50 60 70
MPSAKQRGSKGGHGAASPSEKGKHPGGADDVAKKPPAPQQPPPPAPHRQQHQ-PQHQRNQAHKGHGRG
80 90 100 110 120 130 140
G3GGGKSSSS--SSASAAAASSASSASCRRRLGRAINFELFLYALVRAAFSGNCVHRYLEEVQVRSHQ
Q1QNGSSSTSPNTDHAONSVTAPSPYQPS-STFDAL--SPSPATPSNTDYPG--PHSFEDVSSQGSTAKS
30 40 50 60 70 80 90
X MYLENNAQATQFSPEROYNTGILNMDQ

100 110 120 130 140 150 160 170 180 190 200
PSHLIRVEGNSHAQYVEDITGRGSVLYVPEPPQVGIERT----TVL-YNFMCNSSCVGGMNRRLPILLI-
210 220 230 240 250 260 270 280 290
NEIL-----KDISDGHVVKDARERDFTSLENTVEERLTLTKSINDNIAITFTEVQRSSKEIND
MKAVALSLESESEGKQDLKALKAEVKETQTSAKSREWDMSLARSTLQTMESDITYVEVRELVYLSIKQOOQAFK-
----VTLERTRDG--QVLRRCLEARICAPCGDRKADEDSSRKQVSDSAQNGDAFRQNTGQMTSIKR
270 280 290 300 310 320 330 340
PSHLIRVEGNSHAQYVEDITGRGSVLYVPEPPQVGIERT----TVL-YNFMCNSSCVGGMNRRLPILLI-
170 180 190 200 210 220 230
MKAVALSLESESEGKQDL-KALKAE-VKETQTSAKSREWDMSLARSTLQTMESD-TYVEVRELVLSIKQOOQAFK-
----VTLERTRDG--QVLRRCLEARICAPCGDRKADEDSSRKQVSDSTGDSKRPFRONTIGLQMS
340 350 360 370 380 390 400
AFK-EADTERLAI---QALTEKLUISSEESVSLPPEIRRLLEELRQLKSDSHGPDKEDGGFRHSBAEALQKQSQ
-RSPDDELLVLPVGRETYEMLKIKESLMLQH-TETRQQQQQH----QHLQK--
300 310 320 330 340
OKSODIDS--RLQHVEDGVLSMQVASARQTESLESLSIKSQBHEORLAALQRLGEGLGSSSEADQGLASTV
OK-HLLSACFRNELVLRGEAPTSQDVFRRBSNPPPHSVV
360 370 380 390 X
480 490
RSLGETQVLYGDVEELRS

3. caa49535 (1-602)
US-09-538-106-15 Sequence 15, Application US/09538106
GENERAL INFORMATION:
APPLICANT: MCKEON, FRANK
APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA
APPLICANT: CRUM, CHRISTOPHER
TITLE OF INVENTION: RELATED THERATO
FILE REFERENCE: HMV-038-02
CURRENT APPLICATION NUMBER: US/09/538,106
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/174,493
PRIOR FILING DATE: 1998-10-15
PRIOR APPLICATION NUMBER: 60/087,216
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/062,076
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 7 Optimized Score = 66 Significance = 2.40
Residue Identity = 18% Matches = 93 Mismatches = 296
Gaps = 101 Conservative Substitutions = 0

X MISAKO-----RSGKGHGAAASPSEKGAA-HPSGGADDVAKKPPAPQOPPP
MSQSTQTNFPLSEVQHIMDLEQPCSVQPIDLNFDSESEDGATNKILISMDCIRMQSDLSLDPWMPQY
10 X 20 30 40 50 60 70
50 60 70 80 90 100 110
PPAPHPQHQPHQONQAHGKGSHRGGGGGKSSSS--SSASAAAASSASSASCRRRLGRAINFYLA
TNLGLSLNMDQ-1Q-----GSSSPYNTDAPSPYQPS-STFDAL--SPSP

80 90 100 110 120

1. 120 130 140 150 160 170 180
 LVAAGAFSGWCYHVLEBVQQVRRSHODFSRQREELGQGLOGVEQVQSLQATFGP---FESTIRSSHK-
 I P S N T D V P G - P H S F D V S F Q Q S S T A S T A W Y S T E R - K K Y C Q A K T C P I O I K V M T P P Q O G A V I R A M P Y K K
 130 140 150 160 170 180 190

2. 190 200 210 220 230 240 250
 T P L T K S I N D N I A I F T E V Q R K S O K E I N D M K A V U S L E B E S G N K Q D L - K A L K E A - V K E I Q S A K R E D M E A L
 T V I L - Y N F M C N S S C V G G M R R P I L I I - - - - V T I L E T R D G - Q V L G R R C E A R T C A C P G R D K A D E S D I R K Q
 200 210 220 230 240 250 260

3. 250 260 270 280 290 300 310
 R S T L Q T M E S D - Y T E V R E L V S L K Q E Q A F K - B A C T E R I A L - - Q A L T E K U R S E E S V R L P E B I R R L E E
 Q V S D S T K R P F R O N T H G I M Q M T S I K R R S P D D E L L Y L P V R G R E T Y E M L K U K E S L E M Q L P Q H T E T
 330 340 350 360 370 380 390

4. 320 330 340 350 360 370 380
 L R Q L K D S H G P K E D G G F R H S S A F E A L Q Q K S Q G I D S - - R I Q H E D G V L S M Q V A S A R Q T S L E S L I S K S Q E H E
 Y R Q Q Q Q H - - - - - Q H I L Q K - H L L S A C F R A B I L E V P R R E T K Q S D V F F R I S K P P R S V P
 400 410 420 430 440 450 X

5. 380 390 400 410 420 430 440 X
 Q R L A A L O G R L E G I G S S E A D Q D G I A L S T V R S L G E T Q L V I Y G D V E E L K S

4. caa49535 (1-602)
 US-09-538-106-22 Sequence 22, Application US/09538106
 Sequence 22, Application US/09538106
 GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT: YANG, ANNIE
 APPLICANT: LODA, MASSIMO
 APPLICANT: SIGNORETTI, SABINA
 APPLICANT: CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELLULAR REGULATORY GENES, ENCODED PRODUCTS, AND USES
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 226
 LENGTH: 586
 TYPE: PRT
 ORGANISM: Murine sp.

Initial Score = 6 Optimized Score = 77 Significance = 1.20
 Residue Identity = 19% Matches = 111 Mismatches = 343
 Gaps = 119 Conservative Substitutions = 0

6. X 10
 M P S - - A K O R G S N G G H G A S P S
 X 10
 G L L N S M D Q Q I Q N G S S T S P V N T D H A Q N S V T A P S P V A Q P S S T F D A L S P S A I P S N T D Y P G P H S F D V S F Q Q S T
 30 40 50 60 70 80 90

2. 210 220 230 240 250 260 270
 Q D F S R Q R E B L - - - - G Q G L Q F Q K V Q S L Q A T F G T F F S I L R S S O H K D L T E K A V K O C G S E V R I S E V L
 V G S M R R P I L I V T L E T R D G Q L - G R C F E A R T C A C P G R D K A D E S D I R K Q S C O V S D S A - K N G - - - - D G K R
 220 230 240 250 260 270 280

3. 270 280 290 300 310 320 330
 Q K L Q N E L K D L S G I - H V V K A R E R P T S L E V B E R L T - E L T K - - - - S I N D N I A I F T - E V O K E S Q
 P F R O N - - - - T H G I Q M T S I K R R S P D D E L L Y L P V R G R E T Y E M L K U K E S L E M Q L P Q H T E T R Q Q O C Q
 290 300 310 320 330 340

4. 340 350 360 370 380 390 400
 K E L N D M K A V U S L E E S S N - K D L K A U K L E V A K E Y I Q S A K R E D M E A L R S T Q T M E S D I V E R E V L S K O E
 Q Q A P K E A A D T E R I - A L O U T E K U R S E S V R L P E B I R R L E E L R O L K S D H G P K E D G G F F R H S E A L Q K
 G T H P M A G D M G N L S P T Q A L P P L - S M P S T S - - - H C T P P P Y P T D C S I V S F L A R I G C S S C L D Y - - - T
 420 430 440 450 460 470

5. 410 420 430 440 450 460 470
 S Q G I D S R L Q H V E D G V L S M - Q V A S A R O T E - - - S L E S L I S K S Q E H - - - B O R L A L O Q - R I E G L G S S E A D Q
 T O G I L T I Y Q - - I E H Y S M D D I A L S L K I P E Q F R H A I W K G I L D R Q L H D F S S P H I L R T P S G A S T V S G S S E T G
 480 490 500 510 520 530 540

6. 470 480 490 500 510 520 530
 D G L A S T V R - S L G S T Q L V I Y G D V E E L K R S V G G L P S T V E S L Q V Q E Q V H T L S Q D Q A Q A R L P P Q D F L D R I S S L
 E R V I D A T E R F T L Q T I S P P R D - E M A D F N P M D S R R N K Q R K I R K E B
 550 560 570 580 X

7. 540 550 560
 D N L K A S V S Q V A E D L K M L R T A V D S V

5. caa49535 (1-602)
 US-09-538-106-16 Sequence 16, Application US/09538106
 Sequence 16, Application US/09538106
 GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT: YANG, ANNIE
 APPLICANT: LODA, MASSIMO
 APPLICANT: SIGNORETTI, SABINA
 APPLICANT: CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELLULAR REGULATORY GENES, ENCODED PRODUCTS, AND USES
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15

NUMBER OF SEO ID NOS: 53

SOFTWARE: Patent in Ver 2.1

SHEET 003 ID NO 16

LENGTH: 586

לירפֿרְעָה : אַתְּ

ORGANISM: Homo sapiens
 Initial Score = 6 Optimized Score = 78 Significance = 1.20
 Residue Identity = 19% Matches = 113 Mismatches = 341
 Gaps = 132 Conservative Substitutions = 0

GENERAL INFORMATION:
APPLICANT: MCKEON, FRANK
APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA
APPLICANT: CRUM, CHRISTOPHER
TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
TITLE OF INVENTION: RELATED THERETO
FILE REFERENCE: HAV-038-02
CURRENT APPLICATION NUMBER: US/09/538,106
CURRENT FILING DATE: 2000-03-29

| | | |
|------|---|---|
| 20 | EGK-----HPSGGADDAKKKPPAPQOPPPPPAPHQHQHPOHQPOQ-----HKGKGGHRRGGGGGGKSSS | MPS-----AKQGSKKGHGAAASPS |
| 30 | SSASA-----SSASCSRRLGALANFLYLVAAAFSGMCVHHLBEVQO-----RRSH | 30 40 50 60 70 80 90 |
| 40 | SREFNEQQIAAPPS-----HLIR-----VEGNSHAQIVEDPITGQSVLVPYPPQVGIEFTTYLNFMCNSC | |
| 50 | AKSATWTTSTELKLYCIAKTCPIQIKMTPP-----QAVTRAMPVKKRABHVTTEVVKRCFHNL | |
| 60 | 100 110 120 130 140 150 160 170 180 190 200 210 | 100 110 120 130 140 150 160 170 180 190 200 210 |
| 70 | QDFSRQRRL-----GOGIQLQEVKQVSLQATF-----FESTSLRSSHQ-----DLTFRKAVQGESEWRIS | |
| 80 | VGGNNRRRILIVTLETRDGQVJ-----GRRFEARCACPQRDRKADEDSRKQQVSDST-----RNG-----DG | |
| 90 | 210 220 230 240 250 260 270 | 210 220 230 240 250 260 270 |
| 100 | EVLQKLOQMBILKQDGT-----HVKQARREDPFTSLENTEVERLT-----ELTK-----SINDVIAIFT-EVQK | |
| 110 | TKRPFRRON-----THGQMTSIIKKRSPDDELILYLPYGRERYEMLKKIKESLELMOYLPOHTIERYRQOO | |
| 120 | 280 290 300 310 320 330 340 | 280 290 300 310 320 330 340 |
| 130 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 140 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 150 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 160 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 170 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 180 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 190 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 200 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 210 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 220 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 230 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 240 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 250 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 260 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 270 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 280 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 290 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 300 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 310 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 320 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 330 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 340 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 350 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 360 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 370 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 380 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 390 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 400 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 410 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 420 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 430 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 440 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 450 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 460 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 470 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 480 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 490 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 500 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 510 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 520 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 530 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 540 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 550 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 560 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 570 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 580 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 590 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 600 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 610 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 620 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 630 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 640 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 650 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 660 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 670 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 680 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 690 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 700 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 710 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 720 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 730 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 740 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 750 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 760 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 770 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 780 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 790 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 800 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 810 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 820 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 830 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 840 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 850 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 860 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 870 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 880 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 890 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 900 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 910 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 920 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 930 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 940 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 950 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |
| 960 | 330 340 350 360 370 380 390 400 | 330 340 350 360 370 380 390 400 |
| 970 | 300 310 320 330 340 350 360 370 | 300 310 320 330 340 350 360 370 |
| 980 | RSQKEIINMDKAVASL-----SEGN-----KDQIKAKEVKEIQTSAKREMDMAEST-----LQTMEDDITYRELV | |
| 990 | QDQHQHLLQKQTSIQSPRSYGNSSPPLNNNSMKLPSVQSLINPQQRNALTPTTIPDGGMGANI----- | |
| 1000 | 350 360 370 380 390 400 | 350 360 370 380 390 400 |

PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
 LENGTH: 641
 TYPE: PRT
 ORGANISM: Homo sapiens

PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087, 216
 PRIOR FILING DATE: 1998-05-29
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 Q ID NO 13
 LENGTH: 641
 TYPE: PRT
 ORGANISM: Homo sapiens

| | | | | | | |
|--|----------------------------|---------------------|-----|-----|-----|-----|
| trial Score = 6 | Optimized Score = 78 | Significance = 1.20 | | | | |
| idue Identity = 19% | Matches = 113 | Mismatches = 341 | | | | |
| IDE | Conservative Substitutions | | | | | |
| | X | 10 | | | | |
| GLNSMDQIQNGSSSTSPVNPDHAQNSVTPSPYAQPSSTPDALSPSPAI | MPS--AKQRGSKGHHGAASPS | | | | | |
| 80 | X | 130 | | | | |
| ERKA-----HPGGADDAVKKKPPAPQQPPPPAPHQHQHQHQFQNQA | --HGKGHHGGGGGGKSSSS | | | | | |
| 90 | | | | | | |
| AKSATWYSTEKKLQCQIAKTCPIQIKWMPPP-----QGAVITRAMPVYKCAEHNTVEWVKRCCPNHL | | | | | | |
| 100 | | | | | | |
| 150 | 160 | 170 | 180 | 190 | 200 | 210 |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 |
| SSASAAAAAASSASSASCRRRGRAINFLYFLALVAAASGWCVHNVLEBVQV | -----RSH | | | | | |
| SRBFNEGOIAPPS-----HLIR-VEGNASHAQYVEDPTGRCQSYLVPPFPPQQTETFTVLYNFCNNSC | | | | | | |
| 220 | 230 | 240 | 250 | 260 | 270 | 280 |
| 290 | 300 | 310 | 320 | 330 | 340 | 350 |
| 150 | 160 | 170 | 180 | 190 | 200 | 210 |
| QDFSRQREEL-----GQGLQYBQKVOSLQATFGTRESILASSQHQ--DUTEKAVKQGESEVRIS | | | | | | |
| VGGMNRPLILITVLTFRDQVLT-GRCFEARICACGFRKADSDIRKQVSDST-----KNG-----DG | | | | | | |
| 340 | 350 | 360 | 370 | 380 | 390 | 400 |

6. Ca49535 (1-602) US-09-538-106-13 Sequence 13, Application US/09538106

Sequence 13, Application US/09538106

80 90 90 100 110 110 120
 SSSS-SSSSA AAAAASSSSACSRRLGRAGNLFYIALVAAFSGWCVTHVILBEVQDVRSHODFSQRR
 SSSTSPYNTDHAQNSVTAPSSPAQPS-STFDAL-SPSPALPNTDQG-PHSDVSPQOSSTAKSATWYIS
 130 140 150 160 170 180 190 200 210
 EELQGQIQCQVEQRQSLQMTG---FESILRSQH-QDLTEKAVQGESEVRISEVQLOKQNEI---
 TEL-KKLYQIAKTCPIOKUWTPPPQGAVIRAMPVYKKAETVEVKRCPHESREFNGQIAPPShLIR
 200 210 220 230 240 250 260
 -----KJLSDGJHNVKDRB---RDT-SLEN---TVEREJTELTKSINNIAITFEVORS
 VEGNISHAQYVEDITGROSIVVYEPQVGTSBTIVLNFMONSCVGGMNRPIILIVTETRGQVLR
 270 280 290 300 310 320 330
 QKEINDMKAQVASELESQGNKQDLKAIKEAWEIQLAKSREWDMEALRSLQTMSDIVEVSQKEL
 CFE-----ARTCACPG---RDRKA-DEDSIRKQVSDSAKNGDGTKRPPRQ----NTHGICQTSK---
 340 350 360 370 380 390 400
 QQAFAKEAANDTERIAL---QALTEKLURSSESVSLRPEEEFLRQKPSDASHGPKEGDGRFHS
 ---KRRSPDDELYLPLVVRGRETVEMLKLKIKESPELMOYLPQHNTIETYRQOOOOQH---QHLLQKOTS
 400 410 420 430 440 450 460
 QKQSQGLDLSRQLHQEDGJLISMQYASAROTESLSSLRSQEHBLRA-----ALQGRLEGQSSEAD
 SOSYGNSSPPLNGNSMKLPSUSQLINPQQRNALPTTMFBGMGANIPMGTHMAGMDNGLSPQALP
 460 470 480 490 500 510 520
 DGLASTVSLGETOIVLQGDEVEILKRSVGEELPVTESIQLQKVQBVQHNTLSSQDQQAARLPPD
 PPI-SMPSTSHCTPPPPY-----PTDCSIVRIVQW
 530 540 550 X
 NLKASVSVQTEADLKLRT

```
> O <
O | O IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
Results file 833377.res made by bshears on Wed 9 Jun 104 10:09:36-PDT.

Query sequence being compared: 833377 (1-601)
Number of sequences searched: 12
Number of scores above cutoff: 12

Results of the initial comparison of 833377 (1-601) with:

File : /home/bshears/new.pep

100-

90-

80-

70-

60-

50-

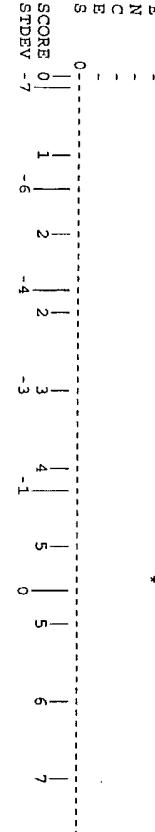
40-

30-

20-

10-

0-



PARAMETERS

| | |
|---------------------|---------|
| Similarity matrix | Unitary |
| Mismatch Penalty | 1 |
| Gap penalty | 1.00 |
| Gap size penalty | 0.05 |
| Cutoff score | 0 |
| Randomization group | 0 |

SEARCH STATISTICS

| | | | |
|---------|-------------|-------------|--------------------|
| Scores: | Mean | Median | Standard Deviation |
| Times: | 00:00:00.00 | 00:00:00.00 | Total Elapsed |

Number of residues: 6199
Number of sequences searched: 12
Number of scores above cutoff: 12

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

| Sequence Name | Description | Length | Init. Score | Opt. Score | Score | Sig. | Frame |
|----------------------|---|--------|-------------|------------|-------|------|-------|
| 1. US-09-538-106-24 | 1 standard deviation above mean **** | 389 | 7 | 61 | 1.39 | 0 | |
| 2. US-09-538-106-18 | Sequence 24, Application | 393 | 7 | 61 | 1.39 | 0 | |
| 3. US-09-538-106-15 | Sequence 15, Application | 448 | 7 | 66 | 1.39 | 0 | |
| 4. US-09-538-106-21 | Sequence 21, Application | 483 | 7 | 66 | 1.39 | 0 | |
| 5. US-09-538-106-23 | **** 0 standard deviation from mean *** | 461 | 6 | 58 | 0.00 | 0 | |
| 6. US-09-538-106-17 | Sequence 17, Application | 461 | 6 | 58 | 0.00 | 0 | |
| 7. US-09-538-106-22 | Sequence 22, Application | 586 | 6 | 79 | 0.00 | 0 | |
| 8. US-09-538-106-16 | Sequence 16, Application | 586 | 6 | 78 | 0.00 | 0 | |
| 9. US-09-538-106-13 | Sequence 13, Application | 611 | 6 | 78 | 0.00 | 0 | |
| 10. US-09-538-106-19 | Sequence 19, Application | 680 | 6 | 79 | 0.00 | 0 | |
| 11. US-09-538-106-14 | **** 1 standard deviation below mean **** | 516 | 5 | 75 | -1.39 | 0 | |
| 12. US-09-538-106-20 | Sequence 20, Application | 555 | 5 | 76 | -1.39 | 0 | |

1. 833377 (1-601)
US-09-538-106-24 Sequence 24, Application US/09538106

Sequence 24, Application US/09538106

GENERAL INFORMATION:

APPLICANT: MCKEON, FRANK

APPLICANT: YANG, ANNIE

APPLICANT: LODA, MASSIMO

APPLICANT: SIGNORETTI, SABINA

APPLICANT: CRUM, CHRISTOPHER

TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES

FILE REFERENCE: HMM-038-02

CURRENT APPLICATION NUMBER: US/09-538-106

PRIOR APPLICATION NUMBER: 09-174,493

PRIOR FILING DATE: 1998-10-15

PRIOR APPLICATION NUMBER: 60/087,216

PRIOR FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 60/062,076

PRIOR FILING DATE: 1997-10-15

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 24

LENGTH: 389

TYPE: PRT

ORGANISM: Murine sp.

Initial Score = 7

Optimized Score = 61

Significance = 1.39

Residue Identity = 188

Matches = 80

Mismatches = 281

Conservative Substitutions = 0

Gaps = 0

X = 50

50 = 60

60 = 70

70 = 80

80 = 90

90 = 100

100 = 110

110 = 120

120 = 130

130 = 140

140 = 150

150 = 160

160 = 170

170 = 180

180 = 190

190 = 200

200 = 210

210 = 220

220 = 230

230 = 240

240 = 250

250 = 260

260 = 270

GGGGGKSSSS--SSASAMMAASSASSCRRLGRALNFIYFLALVAAPAFSGNCVHHLTEVQVRSHQ
QIQLQSSSTSPTNTDAHQNSTTAPSPYQPS-STPDAL--SPSPAIPISTYPG--PHSFDVSIQOSSTAKS
30 40 50 60 70 80 90

DFSRQRFLIGQIQLQGVQVLSQATFGT--FESILRSQHK--QDLTAKVAKVKGESEVRISEVQKQ
ATWYTSFL-KKLYCQAKTPIQIKMTPRPPQGAVTRAMPVYKQHEVTHVVKRCPNHLRSRNEQGQAP
100 110 120 130 140 150 160

NEIL-----KDLSDGIIHVVKDARRFSLNTVEERLTLSKINDNIAIFTEVQKSQETND

PSHLIRVEGNSHAQYVEDPITQRQSVLVPFPPQVGETF---TVL-YNFMNCNSCUGGMRRPILII-
 170 180 190 200 210 220 230
 270 280 290 300 310 320 330
 MCKVASLESEBNKODLKALKEAVKEIQTSAKSREMDMEALRSTIQTMSDITVEVLVLSLKQEQQAFK-
 ---VTELETRIG---OVLGRRCFEARICAPGRDRKADESIRKQVSDSAKNGDAFRONTHGIQMTSIKR
 240 250 260 270 280 290
 RSPDDLELYLPVRGRTYEMLKIKSLELMQYLQHTIETYRQQQQH---QHLLQK--
 300 310 320 330 340
 RSPDDLELYLPVRGRTYEMLKIKSLELMQYLQHTIETYRQQQQH---QHLLQK--
 340 350 360 370 380 390 400
 EADTERL---QALTEKLRSSESVSRUPEEIRRLQKSDSHGP-KEDGGRHSEAFALQKSQ
 410 420 430 440 X 450 460 470
 GUDS---RLOHVEDGVLMSMQVASAROTESLESLLSKSQEHEQRLLAPAGALEGLGSSEADQDGLASTV
 480 490
 HLLSACPRNELVEPRTEGAPTOQSDVFRHSNPPNHSVY X
 TQLVLYGDVVEELKRSV

2. 533377 (1-601)
 US-09-538-106-18 Sequence 18, Application US/09538106
 GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT: YANG, ANNIE
 APPLICANT: LODA, MASSIMO
 APPLICANT: SIGNORETTI, SABINA
 APPLICANT: CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 FILE REFERENCE: HNV-038.02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: Patentin Ver. 2.1
 S50 ID NO: 18
 LENGTH: 393
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score = 7 Residue Identity = 19% Gaps = 69
 Optimized Score = 30保守型 Substitutions = 30
 Significance = 1.39 Mismatches = 278
 Length: 448

MPSAKQRGSKKGHGAASPSEKGKAHPGGADDVAKKPPAPQQPPAPHQHQHQHQHQHQKGRG
 10 20 30 40 X 50 60 70
 MLYIENNAAATQFSEPBQYINGLANSMDQ
 X 10 20

Initial Score = 7 Residue Identity = 18% Gaps = 101
 Optimized Score = 30保守型 Substitutions = 93
 Significance = 1.39 Mismatches = 296
 Length: 448

MPSAKQ---RGSKGHGASPSRGA---HPSGGADDVAKKPPAPQQPP
 10 X 20 30 40 50
 MSQSTQNEFLSPVFEQHDFLEQPCIQVQPIDLNFDPEPSDGAATKIEISMDCIRMODSLSDPWPQY
 50 60 70 80 90 100
 PPAPFHQHQHQHQAHGKGHHGGGGKSSS -SASASAAASSASSCSRRLGRAINFLFLA
 TNGLANSMDQ-ION-----GSSTSPNTDRAONSYTAPYQAPS-STFDAL-SPSP
 80 90 100 110 120

120 130 140 150 160 170 180
 LVAIAAFSCWCVHVLERVQVRSHQDFSRQRELGOGLOVEQKVQSLQATFGT---FESTIRSSHK-
 IPNTDYG--PISFDVSFQOSSAKSATWTYSTEKLKLYCQIAKCPQIKWMPPQGAVIRAMPVKK
 130 140 150 160 170 180 190

190 200 210 220 230 240 250
 -QDLTEKAVKVGSESEVSVIQLQNEIL---KDLSDGIVHVKDARERDFTSLENTVERL
 AEVTEVVKRCRPHELSERFNEQIAIPSPHSLIRVEGNSHAQYQVEDDITGROSULVYEPPOVGTFT---
 200 210 220 230 240 250 260

250 260 270 280 290 300 310
 TELTKSINDNIAIPTEVOKRSQKEINIMKAVASLESEGENKODI-KALKEN-AVKEIQTSAKREWDMAL
 QVNSDTSKNGDGTTRPFRONTGQIOMTSIKRKRSPDDELLYLIVPVRGRTBYEMILKIKESLIMQYIPOHIT
 270 280 290 300 310 320 330
 320 330 340 350 360 370 380
 RSTLQTMESD-IVTEVRLVLSKQEOQAFK-EADDERL---QALTEKLRSEBESVRLPBBIRLLEE
 IROQKSPSHGPKEDDGFRHSEAFALQOKSGQLS---RLQHVEDGVLSMQVASARQTESLESLSKQSH
 YRQQQQOHH---QHILQK-HILSACFRNLVEPRTPKQSDVFRISKPPNSVY
 330 340 350 360 370 380 390
 400 410 420 430 440 X
 450 460 470 480 490
 ORLAPAGALEGLGSSSEADQDGLASTVRSLGETOQLVLYGDVEELKRSV

150 160 170 180 190 200 210
 EELQGQLQVEQKVQSLQATFGT---FESTIRSSHK-QDLTEKAVKVGSESEVSVIQLQNEIL-
 TEL-KKLYCQIAKCPQIKWMPPQGAVIRAMPVTKAHTEVVKRCRPHELSERFNEQIAIPSPHSLR
 200 210 220 230 240 250 260
 220 230 240 250 260 270 280
 280 290 300 310 320 330 340
 SLESEGENKODIKAKEVKEIQLTSKASREMEALRSLTQMTESDIBIYTEVRLVLSKQEOQAFK-EADDE
 TLERD---QVLRGRCFARICACPGDRKADEDSIRKQQVSDSAKNGDAFRONTGQIOMTSIKRSPDDE
 330 340 350 360 370 380 390
 350 360 370 380 390 400 410
 RLAI---QALTEKLRSEBESVRLPBBIRLLEEOKRSKEDGFRHSEAFALQOKSGQLS---
 LLVLPVRGRTBYEMILKIKESLIMQYIPOHITRQQQQH---QHILQK-HILSAC
 400 410 420 430 440 X
 450 460 470 480 X
 490
 GDVEELKRSV

4. S33377 (1-601) Sequence 21, Application US/09538106
 Sequence 21, Application US/09538106
 GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT: YANG, ANNIE
 APPLICANT: LODA, MASSIMO
 APPLICANT: SIGNORETTI, SABINA
 APPLICANT: CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538.106
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 483
 TYPE: PRT
 ORGANISM: Murine sp.

Initial Score = 7 Optimized Score = 66 Significance = 1.39
 Residue Identity = 18% Matches = 90 Mismatches = 299
 Gaps = 97 Conservative Substitutions = 0

X MPSAKQ-----RGSK
 X MPSAKQ-----RGSK
 5. S33377 (1-601) Sequence 23, Application US/09538106
 Sequence 23, Application US/09538106
 GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT: YANG, ANNIE
 APPLICANT: LODA, MASSIMO
 APPLICANT: SIGNORETTI, SABINA
 APPLICANT: CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538.106
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 461
 TYPE: PRT
 ORGANISM: Murine sp.

MNPETSRCAIQYCPDPYIQRIFIETPAHFSKESYVRSAMSQSTOTSERLSPPEVQHIMDPLSQPICSVQPI
 10 20 30 40 50 60 70
 MNFETSRCAIQYCPDPYIQRIFIETPAHFSKESYVRSAMSQSTOTSERLSPPEVQHIMDPLSQPICSVQPI
 10 20 30 40 50 60 70

Initial Score = 6
 Residue Identity = 18
 Gaps = 89
 Optimized Score = 58
 Matches = 81
 Conservative Substitutions = 260
 Significance = 0.00
 Mismatches = 260

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens

GLNSMDQIQNGSSSTSPTNTDHAQNUTTAPSPYQAPSSTFDALSPSPALIPSTVDFGPHSPFVFSQGST
MPS--AKORGSKGHGAGS
X

| | | | | | |
|--------------------|-----|------------------------------|----|----------------|------|
| Initial Score = | 6 | Optimized Score = | 58 | Significance = | 0.00 |
| Residue Identity = | 18% | Matches = | 82 | Mismatches = | 255 |
| Gaps = | 99 | Conservative Substitutions = | 0 | | |

| | | | | | | |
|--|---|-----|-----|-----|-----|----|
| 0 | 30 | 40 | 50 | 60 | 70 | 80 |
| LEKGA-----HPGGADDVAKKPPAPQQPPPPAPAPHQOQHPOHQDQ-----HKGCHRGGGGGGKSSSS | AKSATWTTSTELKLYCQIAKTCPIQIKMTPP-----OGAVIRAMPYKKAEBIVTEVKRKPNH | EL | | | | |
| 100 | 110 | 120 | 130 | 140 | 150 | |
| SSASAAAAAAASSSSASCSSRRLGRALNLFYLALVAAKAFSGMVCVHILEVQOV-----RRSH | SRFPNEQQIAPPS-----HLIR-----VEGNHSQAYVEDPTGQSOLVLPYEPQVGTEFTTYLNFMCNSC | | | | | |
| 90 | 100 | 110 | 120 | 130 | 140 | |
| 160 | 170 | 180 | 190 | 200 | 210 | |

QDFSRQLEL-----GQGIGQVECKVQSIQATQFESTLRSQHQDQDLTEKARQGSESVRSIESEVL
 VGGMRNRRRLLITLTERPDGQVL-GRRPEEARCACFQRDRKAEDSIRKQQVSDA-KNG-----DGTR
 220
 230
 240
 250
 260
 270
 280
 290
 300
 310
 320
 330
 340
 350
 360
 370
 380
 390
 400
 410
 420
 430
 440
 450
 460

OKLQNEELKLDSDLGI-HAVKDAERDTSLENTVEELT-BLTK-----SINDIAFT-EVQKRSQ
 PFRQN-----HGIQWMSIKERSPPDLYIPVGRGRETVEYMLKIKESLIMQVLPQHTEVYRQQQQ
 210
 220
 230
 240
 250
 260
 270
 280
 290
 300
 310
 320
 330
 340
 350
 360
 370
 380
 390
 400
 410
 420
 430
 440
 450
 460

KEINDMKAKVAVSLEEESEN-KQDILAKALEKAVKRIQTSKSRENDMEARLSTLQTMESDITYEVRELNSLKQE
 HCHLLOQKOTSMWSQSYYGNSSPPLNKMDMSNMKUPSVSOLQINPOQRNAU-TPTM-----PEGMGNIPMM
 270
 280
 290
 300
 310
 320
 330
 340
 350
 360
 370
 380
 390
 400
 410
 420
 430
 440
 450
 460

QQAFAKEADTERL-ALQOLITEKULRSSESVSRLPPEERLLEBLRQKSDSHOPKEDGCFRHSAFAELQK
 GTHMPMAGDMGLSPTOALIPPLPMSPTSHCTPPPPPTDCSIVRQVY
 340
 350
 360
 370
 380
 X
 390
 400
 410

SSSAAGAAAGAASSASSASCKRKGALFLFLYALVAAAFSGCWVHVVLEQV-----KKP
 SREPNEQGIAPPS-----HLIR-----WEGNSHAQVVEDPITGRQSVTVPVPPQGTEFTWLYNFCNSCC
 160
 QDFSRQZBELL-----GQGLOGYFQKVQVSQATGGFTFSILRSQHKO---DLEKAVKQGESEVSRIS
 VGGNNRBRPILITVLTBRDQYL-GRCFBEARICAGPGRDKAKADESSIRKQVSST-----KNG-----DCC
 220
 230 240 250 260 270
 EVLQKLUONEILKUDS3I-HVVKDARERDFTSLENTEVEILT-BLK-----SINDIAIFT-EVQK
 TKEPFRON-----THQWMSIKKERSPDDBELLYPVRGRGTYEMILKIKESLELMQYLPOHTIETYRQOC
 280
 290 300 310 320 330 340
 RSQEINNDKAVASLESEEN-KDQKALKEAVKELQTSKRENDMEAIRST-LQTMWSIDYREVRELVA
 QDQHQHQLQKQTSIOPSSYGNSSPPLANKOMSKWFLSVQSLINPOORNALTPPT-PDGMGANI-----
 350 360 370 380 390 400

6. s33377 (1-601)
US-09-53817 Sequence 17, Application US/09538106
Sequence 17, Application US/09538106
GENERAL INFORMATION:

ALQQKSQGLDSRLQHVEDGVLSMQVASARQTE
410 420 430

APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA

Sequence 22, Application US/09538106

TITLE OF INVENTION: CELL REGULATORY
TITLE OF INVENTION: RELATED THERETO
FILE REFERENCE: HNV-038-02
CURRENT APPLICATION NUMBER: US/09/53333
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/174,493
PRIOR FILING DATE: 1998-10-15
PRIOR APPLICATION NUMBER: 60/187,216
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/062,076
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ. NOs: 53

APPLICANT: MCKEON, FRANK
APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA
APPLICANT: CRIM, CHRISTOPHER
TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
TITLE OF INVENTION: RELATED THERETO
FILE REFERENCE: HMV-038-02
CURRENT APPLICATION NUMBER: US/09/538,106
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/174,493
DPTO. FILING DATE: 1998-10-15

| | |
|---|-----|
| EVOKLQNLNTEILKBDLSDG-----HVTQDARERDFTSLENTVEERLT-----ELTK-----SINDNIAIFT-EVOK | 210 |
| TKRDPQRN-----THGQMTSTKRRNSPPDDELLYLWVRGRITTYEMULKIKESLELMQYLOHTIETYRQQQ | 220 |
| 340 | 230 |
| RSQKEBNDMKAYASLESEGN-KQDLKALKAVKE-TQTSAKSREMDMEARST-LQTMISDITYEVRELV | 240 |
| QQQHOHLLQKQTSTQSPSYGNSSPPUNKNSMNKLPSVSLQINPOQORNALJPTTIDPGMGANI----- | 250 |
| 410 | 260 |
| 270 | 270 |
| RSQKEBNDMKAYASLESEGN-KQDLKALKAVKE-TQTSAKSREMDMEARST-LQTMISDITYEVRELV | 280 |
| QQQHOHLLQKQTSTQSPSYGNSSPPUNKNSMNKLPSVSLQINPOQORNALJPTTIDPGMGANI----- | 290 |
| 410 | 300 |
| 420 | 310 |
| 430 | 320 |
| 440 | 330 |
| 450 | 340 |
| 460 | 350 |
| SLKQEQQAFKAEDTERL-ALQALTEKULRSBVSRLPESIRRLBELLRQLKSDHGPKEQDGFRHSEAF | 360 |
| --PHMGTMHFMAGDMMNGSPTQALPPPU-SMPS-----HCTPPPPRYPDCTSIVSFLARLGCCSCLDYF- | 370 |
| 470 | 380 |
| 480 | 390 |
| 490 | 400 |
| 500 | 410 |
| 510 | 420 |
| 520 | 430 |

Sequence 13, Application US/09538106 US-09-550-106-13 Sequence 13, Application US/09538106
GENERAL INFORMATION:
APPLICANT: MCKEON, FRANK
APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA
APPLICANT: CRUM, CHRISTOPHER
TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
TITLE OF INVENTION: RELATED THERETO
FILE REFERENCE: HMY-038.02
CURRENT APPLICATION NUMBER: US/09/538,106
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/174,493
PRIOR FILING DATE: 1998-10-15

ALQQKSGQGLDRLQHEDGVLSM-QVASARQE---SLESLSQSQEHRQLARAGALBGLGSSEADQDG
 410
 ----TMOGLITIYQ---IERSYMDLIAKSQPEFRHAIWKGILDRQHLB-FSSPSHLRTPSS-----
 420
 530
 540
 550
 560
 570
 580
 LASTV-RLSLGERQLVYGD-VEELKESVGEPLSTWESLQVKQBEQHTLISQDQAQARLPPQDFLDRSSL
 470
 480
 490
 500
 510
 520
 X
 530
 -ASTVUFGSSSTRGERBVIDAVRFTLQQTISFPPRDBWNDFNDMDARRNKGQRKIXEGE
 590
 600
 610
 620
 630
 640
 NILKASTVSQVEADLKMURTAVIDSLVAVSKIEBTNEMLI
 540
 550
 560
 570

PRIOR APPLICATION NUMBER: 60/087,216
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/062,076
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
Initial Score = 6 Optimized Score
Residue Identity = 19% Matches
Gaps = 131 Conservative Substitutions

| | |
|---|---|
| X MPS --- AKORGSKKGHGGRAPS GLNSMDQQI QNGSSSTSPYNTDHAQNSVTA PSPYAQPSSTFDALSPSPALP S PSLTDYFOPHSIDVFSQOST X 80 90 100 110 120 130 140 | X 0 10 20 30 40 50 60 70 80 90 100 110 120 130 140 |
| AKSATWYTSPELKLYCQIAKTCPIQIKVNTTPP ----- QGAVIRAMPVYKKAHUTEVVKRCNHEL 150 160 170 180 190 200 210 | 150 160 170 180 190 200 210 |
| BKGA ----- HPSGGADDVAKKPPPAFQQPPPFAPHPQOQHPQOHPQO NA --- HKGKGGRRGGGGGGKSSSS 10 30 40 50 60 70 80 90 100 110 120 130 140 | 10 30 40 50 60 70 80 90 100 110 120 130 140 |

CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09174, 493
PRIOR FILING DATE: 1998-10-15
PRIOR APPLICATION NUMBER: 60/087, 216
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/062, 076
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 19
LENGTH: 680
TYPE: PRT

| | | | | | | |
|---|-----|-----|-----|-----|-----|-----|
| SSASASASASASASASCSRRGLGRALNPFYLYALVAAAFSGWCVHHVTEVQOV-----RRSH | 90 | 100 | 110 | 120 | 130 | 140 |
| SREFNEQIIPPS-----HLIR-----VEGNSHAQYVEDITITGROSIVLYPPEPPQVGTPFTIVLYNFCNSC | 220 | 230 | 240 | 250 | 260 | 270 |
| QDFSRQREEE-----GOGLOCVEQVKQVOSLQTFGFGFESTILRSQHQQ-----DLTEKAVKQGESEVRSI | 150 | 160 | 170 | 180 | 190 | 200 |
| VGGMARRPILIVTLETRDQVL-----GRCEBEEARICAGCPGSDRKADEDSRRQQVSDST-----XNG-----DG | 280 | 290 | 300 | 310 | 320 | 330 |

ORGANISM: Murine sp.

| | | | | | |
|--------------------|-----|------------------------------|-----|----------------|------|
| Initial Score = | 6 | Optimized Score = | 79 | Significance = | 0.00 |
| Residue Identity = | 19% | Matches = | 113 | Mismatches = | 339 |
| Gaps = | 122 | Conservative Substitutions = | 0 | | |

X 10
MPS--AKQRGSKGGIGAASPS
|
GLNSMDQQIONGSSSTSPTDHAQNSVTAPSPTVQPSSTFDALSPSPAIAPSNTDYPGPHSFVDYFQQSST
120 130 140 150 160 X 170 180

NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 516
TYPE: PRT
ORGANISM: *Homo sapiens*

| | | | | | |
|--------------------|-----|------------------------------|-----|----------------|-------|
| Initial Score = | 5 | Optimized Score = | 75 | Significance = | -1.39 |
| Residue Identity = | 18% | Matches = | 105 | Mismatches = | 336 |
| Gaps = | 127 | Conservative Substitutions = | 0 | | |

QDPSRQEED-----GEOLOGEBOKVOSIQAFGFTFESILSSOHQDLSKAVKOGESEVSRISVNL
 VGGMNRPLILITVLETRDGQVL-GRRCFEARICAGPGRDKADESDIRQQVSDSA-KNG-----DGTRR
 320 330 340 350 360 370
 210 220 230 240 250 260
 OKLONBILKUDLSGDI--HVVVDARERDFTSILENTVERLT--ELTK-----SINDNIAIFT-EVQRKSQ
 PFRON-----THGIQMTSICKRRSPDDELIVLPVRGRETTEMILKISELMLMQLPQHTIETYRQQQQQ
 380 390 400 410 420 430 440

MPSAKO-----RGSKGHGAAASSEKGK --- HPGGGADDVAKKKPPPPQQQPP
 MSQSTQTMFLSIEVFQHIIWDFLEQPICSVQPIIDLNFDVDESESDGATNKHISMDCTRMPSDLSDPWMQY
 10 X 20 30 40 50 60 70
 PPAHSPQHQPHQHPRQHNGKGKGGGGGKSSSS -SSASA AAAAASSSSACSSRRUGRAINFLFYLA
 TNLGLNNNDQQ-IQN-----GSSSTSPYNTDHAQNSVTABSPYAOPS-STFDAL-SPSPA
 80 90 100 110 120

KEINDMKAKVASLEESBN-KQDLKALKEAVKEIQTSAKRREWDMEARLSTIQTMSDITYTEVREBLUSLKQE
HQHLIQLQTSWQSOSQSYGNSSPPLNKNSMKLPSVSLNQPQRNAL---TPTM-----PEGNANTPMM
450 460 470 480 490 500

120
 130
 140
 150
 160
 170
 180
 190
 200
 LVAAGAAFGWCVHVBLEBVOYRSHDFFRSRREBQGQLOGVEQKVSQLOAFTG---FESILRSQHK-
 IPSNTDYF---PHSFDVSSQOOSTAKATWVYSTEL-KLYCQIAKCPICPQIKWMPQPGAVIRAMPVYKK
 130
 140
 150
 160
 170
 180
 190
 200

QQAEKADDELLR-ALQALI-ELKLUKSEESVSRILPEBIRRLFEEELRQLKSDSHGPEDGGRHSEAFALQK
 GTHMPWMAGDNLGNSLPTQALPPPL--SMPSTS-----HCTPPPPYTDCCSVSFLARLGESSCQDF-----T
 510 520 530 540 550 560

470 480 490 500 X 520 530
SOGJUSLJOWEDGVISM-UVASAROTESLILSK-----SPEHEOCLAPACA-LUGGIGSBAD
TOGLITTIQ--IEHYSWMDLASKTPEQFRHAINGKILDHQRQLDFSSPPHLR-TPSCASTVSGSBR
570 580 590 600 610 620 630

-----TVEERLFLTKESINDIAIAITFENQRSQKINDMGAKVASLESEGNKODIKALKAEVKEIQTSAK
 FMCNSSCVGGMARRPILITVLTETRDQVLRRCFE-----ARICACFG-----RDRKA-----DEDSIRKQQVSD
 270 280 290 300 310 320
 310 320 330 340 350 360

GERVDAVFTLROTISFPPRD--IWNDNFNFMDSSRRNKOQRIKERGE
640 650 660 670 680
540 550 560
LDNLKASVSVQEAUDLKLRTAVDSL

STKNGDGKTKRPRO-----NTHGIQMSIK-----KRRSPDDELILYLPVRGRTYEMLLKIKESDELMQYL
 330 340 350 360 370 380
 IRLLEEEERQLQKSDSHGPKEDDGAFGRHSEAAFLQQ--KSGQDLS-----RLQHVEDGVLSNOVATAR
 370 380 390 400 410 420

11. 6333377 (1-601)
US-09-538-106-14 Sequence 14, Application US/09538106

14, application US/09538106
GENERAL INFORMATION:
APPLICANT: MCKEON, FRANK
APPLICANT: YANG, ANNIE
APPLICANT: LODA, MASSIMO
APPLICANT: SIGNORETTI, SABINA
APPLICANT: CRUM, CHRISTOPHER
TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
TITLE OF INVENTION: RELATED THERETO
PARENT APPLICATION NUMBER: PCT/US03/0209
PARENT APPLICATION NUMBER: 106

PTTIDPGANIPMMGCHMPMAGDMGLISPLQALPPPL-SMPSTSHCTPPPPY-----PRDCSIVRI
 460 470 480 490 500 510
 QTESLSLISLKSQEHORLAPAGALEGIGSSBADQGLASLRTSGETQLVYGDVEELKRSVGPPLSTVES
 LOKVQEQVQHTLISQDQAQARLPPQDFLDRLISSLNLIKASVSQVEADLKLRLT
 WQV X

PRIOR APPLICATION NUMBER: 09/174,493
PRIOR FILING DATE: 1998-10-15
PRIOR APPLICATION NUMBER: 60/087,216

12. 5333377 (1-601)
US-09-538-106-20 Sequence 20, Application US/09538106

PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-10-15

APPLICANT: YANG, ANNE
 APPLICANT: LODA, MASSIMO
 APPLICANT: SIGNORETTI, SABINA
 APPLICANT: CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 FILE REFERENCE: HNV-038-02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 20
 LENGTH: 555
 ORGANISM: Murine sp.

Initial Score = 5 Optimized Score = 76 Significance = -1.39
 Residue Identity = 18% Matches = 105 Mismatches = 338
 Gaps = 123 Conservative Substitutions = 0

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